

SEQUENCE LISTING

caa atc ctg ggt gtc aaa gcc tct agg ttt ctt tgc caa cag cca gat 337
Gln Ile Leu Gly Val Lys Ala Ser Arg Phe Leu Cys Gln Gln Pro Asp

[illegible]

<400> 2															
Met	Glu	Trp	Met	Arg	Ser	Arg	Val	Gly	Thr	Leu	Gly	Leu	Trp	Val	Arg
1				5					10					15	
Leu	Leu	Leu	Ala	Val	Phe	Leu	Leu	Gly	Val	Tyr	Gln	Ala	Tyr	Pro	Ile
			20					25					30		
Pro	Asp	Ser	Ser	Pro	Leu	Leu	Gln	Phe	Gly	Gly	Gln	Val	Arg	Gln	Arg
		35					40					45			
Tyr	Leu	Tyr	Thr	Asp	Asp	Asp	Gln	Asp	Thr	Glu	Ala	His	Leu	Glu	Ile
	50				55					60					
Arg	Glu	Asp	Gly	Thr	Val	Val	Gly	Ala	Ala	His	Arg	Ser	Pro	Glu	Ser
65					70					75				80	
Leu	Leu	Glu	Leu	Lys	Ala	Leu	Lys	Pro	Gly	Val	Ile	Gln	Ile	Leu	Gly
				85					90				95		
Val	Lys	Ala	Ser	Arg	Phe	Leu	Cys	Gln	Gln	Pro	Asp	Gly	Ala	Leu	Tyr
			100					105					110		
Gly	Ser	Pro	His	Phe	Asp	Pro	Glu	Ala	Cys	Ser	Phe	Arg	Glu	Leu	Leu
		115					120					125			
Leu	Glu	Asp	Gly	Tyr	Asn	Val	Tyr	Gln	Ser	Glu	Ala	His	Gly	Leu	Pro

130	135	140
Leu Arg Leu Pro Gln Lys Asp Ser Pro Asn Gln Asp Ala Thr Ser Trp		
145	150	155
Gly Pro Val Arg Phe Leu Pro Met Pro Gly Leu Leu His Glu Pro Gln		160
	165	170
Asp Gln Ala Gly Phe Leu Pro Pro Glu Pro Pro Asp Val Gly Ser Ser		175
	180	185
Asp Pro Leu Ser Met Val Glu Pro Leu Gln Gly Arg Ser Pro Ser Tyr		190
	195	200
Ala Ser		205
210		

<210> 3
 <211> 643
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (9)...(638)

<400> 3
 agccattg atg gac tcg gac gag acc ggg ttc gag cac tca gga ctg tgg 50
 Met Asp Ser Asp Glu Thr Gly Phe Glu His Ser Gly Leu Trp
 1 5 10

gtt tct gtg ctg gct ggt ctt ctg ctg gga gcc tgc cag gca cac ccc 98
 Val Ser Val Leu Ala Gly Leu Leu Leu Gly Ala Cys Gln Ala His Pro
 15 20 25 30

atc cct gac tcc agt cct ctc ctg caa ttc ggg ggc caa gtc cgg cag 146
 Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly Gly Gln Val Arg Gln
 35 40 45

cgg tac ctc tac aca gat gat gcc cag cag aca gaa gcc cac ctg gag 194
 Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr Glu Ala His Leu Glu
 50 55 60

atc agg gag gat ggg acg gtg ggg ggc gct gct gac cag agc ccc gaa 242
 Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala Asp Gln Ser Pro Glu
 65 70 75

agt ctc ctg cag ctg aaa gcc ttg aag ccg gga gtt att caa atc ttg 290
 Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly Val Ile Gln Ile Leu
 80 85 90

gga gtc aag aca tcc agg ttc ctg tgc cag cgg cca gat ggg gcc ctg 338
 Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg Pro Asp Gly Ala Leu
 95 100 105 110

tat gga tcg ctc cac ttt gac cct gag gcc tgc agc ttc cgg gag ctg 386
 Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys Ser Phe Arg Glu Leu
 115 120 125

205210" 59209001

ctt ctt gag gac gga tac aat gtt tac cag tcc gaa gcc cac ggc ctc 434
 Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu Ala His Gly Leu
 130 135 140
 ccg ctg cac ctg cca ggg aac aag tcc cca cac cgg gac cct gca ccc 482
 Pro Leu His Leu Pro Gly Asn Lys Ser Pro His Arg Asp Pro Ala Pro
 145 150 155
 cga gga cca gct cgc ttc ctg cca cta cca ggc ctg ccc ccc gca ctc 530
 Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly Leu Pro Pro Ala Leu
 160 165 170
 ccg gag cca ccc gga atc ctg gcc ccc cag ccc ccc gat gtg ggc tcc 578
 Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro Pro Asp Val Gly Ser
 175 180 185 190
 tcg gac cct ctg agc atg gtg gga cct tcc cag ggc cga agc ccc agc 626
 Ser Asp Pro Leu Ser Met Val Gly Pro Ser Gln Gly Arg Ser Pro Ser
 195 200 205
 tac gct tcc tga agcca 643
 Tyr Ala Ser *

<210> 4
 <211> 209
 <212> PRT
 <213> Homo sapiens

<400> 4
 Met Asp Ser Asp Glu Thr Gly Phe Glu His Ser Gly Leu Trp Val Ser
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 20 25 30
 Asp Ser Ser Pro Leu Leu Gln Phe Gly Gly Gln Val Arg Gln Arg Tyr
 35 40 45
 Leu Tyr Thr Asp Asp Ala Gln Gln Thr Glu Ala His Leu Glu Ile Arg
 50 55 60
 Glu Asp Gly Thr Val Gly Gly Ala Ala Asp Gln Ser Pro Glu Ser Leu
 65 70 75 80
 Leu Gln Leu Lys Ala Leu Lys Pro Gly Val Ile Gln Ile Leu Gly Val
 85 90 95
 Lys Thr Ser Arg Phe Leu Cys Gln Arg Pro Asp Gly Ala Leu Tyr Gly
 100 105 110
 Ser Leu His Phe Asp Pro Glu Ala Cys Ser Phe Arg Glu Leu Leu Leu
 115 120 125
 Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu Ala His Gly Leu Pro Leu
 130 135 140
 His Leu Pro Gly Asn Lys Ser Pro His Arg Asp Pro Ala Pro Arg Gly
 145 150 155 160
 Pro Ala Arg Phe Leu Pro Leu Pro Gly Leu Pro Pro Ala Leu Pro Glu
 165 170 175

20624059007

Pro Pro Gly Ile Leu Ala Pro Gln Pro Pro Asp Val Gly Ser Ser Asp
 180 185 190
 Pro Leu Ser Met Val Gly Pro Ser Gln Gly Arg Ser Pro Ser Tyr Ala
 195 200 205
 Ser

<210> 5
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer

<400> 5
 agccattgat ggactcggac 20

<210> 6
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer

<400> 6
 tggcttcagg aagcgtagct 20

<210> 7
 <211> 16
 <212> PRT
 <213> Homo sapiens

<400> 7
 Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr Glu Ala His
 1 5 10 15

<210> 8
 <211> 15
 <212> PRT
 <213> Homo sapiens

<400> 8
 His Leu Pro Gly Asn Lys Ser Pro His Arg Asp Pro Ala Pro Arg
 1 5 10 15

<210> 9
 <211> 218
 <212> PRT
 <213> Mus musculus

2062270-5020303T

<400> 9

Met Ala Arg Lys Trp Asn Gly Arg Ala Val Ala Arg Ala Leu Val Leu
 1 5 10 15
 Ala Thr Leu Trp Leu Ala Val Ser Gly Arg Pro Leu Ala Gln Gln Ser
 20 25 30
 Gln Ser Val Ser Asp Glu Asp Pro Leu Phe Leu Tyr Gly Trp Gly Lys
 35 40 45
 Ile Thr Arg Leu Gln Tyr Leu Tyr Ser Ala Gly Pro Tyr Val Ser Asn
 50 55 60
 Cys Phe Leu Arg Ile Arg Ser Asp Gly Ser Val Asp Cys Glu Glu Asp
 65 70 75 80
 Gln Asn Glu Arg Asn Leu Leu Glu Phe Arg Ala Val Ala Leu Lys Thr
 85 90 95
 Ile Ala Ile Lys Asp Val Ser Ser Val Arg Tyr Leu Cys Met Ser Ala
 100 105 110
 Asp Gly Lys Ile Tyr Gly Leu Ile Arg Tyr Ser Glu Glu Asp Cys Thr
 115 120 125
 Phe Arg Glu Glu Met Asp Cys Leu Gly Tyr Asn Gln Tyr Arg Ser Met
 130 135 140
 Lys His His Leu His Ile Ile Phe Ile Gln Ala Lys Pro Arg Glu Gln
 145 150 155 160
 Leu Gln Asp Gln Lys Pro Ser Asn Phe Ile Pro Val Phe His Arg Ser
 165 170 175
 Phe Phe Glu Thr Gly Asp Gln Leu Arg Ser Lys Met Phe Ser Leu Pro
 180 185 190
 Leu Glu Ser Asp Ser Met Asp Pro Phe Arg Met Val Glu Asp Val Asp
 195 200 205
 His Leu Val Lys Ser Pro Ser Phe Gln Lys
 210 215

<210> 10

<211> 216

<212> PRT

<213> Homo sapiens

<400> 10

Met Arg Ser Gly Cys Val Val Val His Val Trp Ile Leu Ala Gly Leu
 1 5 10 15
 Trp Leu Ala Val Ala Gly Arg Pro Leu Ala Phe Ser Asp Ala Gly Pro
 20 25 30
 His Val His Tyr Gly Trp Gly Asp Pro Ile Arg Leu Arg His Leu Tyr
 35 40 45
 Thr Ser Gly Pro His Gly Leu Ser Ser Cys Phe Leu Arg Ile Arg Ala
 50 55 60
 Asp Gly Val Val Asp Cys Ala Arg Gly Gln Ser Ala His Ser Leu Leu
 65 70 75 80
 Glu Ile Lys Ala Val Ala Leu Arg Thr Val Ala Ile Lys Gly Val His
 85 90 95
 Ser Val Arg Tyr Leu Cys Met Gly Ala Asp Gly Lys Met Gln Gly Leu
 100 105 110
 Leu Gln Tyr Ser Glu Glu Asp Cys Ala Phe Glu Glu Glu Ile Arg Pro
 115 120 125

1006036.013900
 2005270.013900

Asp	Gly	Tyr	Asn	Val	Tyr	Arg	Ser	Glu	Lys	His	Arg	Leu	Pro	Val	Ser
130						135					140				
Leu	Ser	Ser	Ala	Lys	Gln	Arg	Gln	Leu	Tyr	Lys	Asn	Arg	Gly	Phe	Leu
145					150					155					160
Pro	Leu	Ser	His	Phe	Leu	Pro	Met	Leu	Pro	Met	Val	Pro	Glu	Glu	Pro
				165					170					175	
Glu	Asp	Leu	Arg	Gly	His	Leu	Glu	Ser	Asp	Met	Phe	Ser	Ser	Pro	Leu
			180					185					190		
Glu	Thr	Asp	Ser	Met	Asp	Pro	Phe	Gly	Leu	Val	Thr	Gly	Leu	Glu	Ala
	195						200					205			
Val	Arg	Ser	Pro	Ser	Phe	Glu	Lys								
210						215									

<210> 11
 <211> 10
 <212> PRT
 <213> Unknown

<220>
 <223> Residues which contain the anitgenic determinant
 recognized by the myc monoclonal antibody.

<400> 11
 Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu
 1 5 10

<210> 12
 <211> 5
 <212> PRT
 <213> Unknown

<220>
 <223> Preferred thrombin cleave site.

<400> 12
 Leu Val Pro Arg Gly
 1 5

<210> 13
 <211> 10
 <212> PRT
 <213> Unknown

<220>
 <223> Residues which bind to paramagnetic streptavidin
 beads (used for purification).

<400> 13
 Ser Ala Trp Arg His Pro Gln Phe Gly Gly
 1 5 10

10060765-042902

<210> 14
<211> 7
<212> PRT
<213> Homo sapiens

<400> 14
Arg Pro Tyr Asp Gly Tyr Asn
1 5

<210> 15
<211> 6
<212> PRT
<213> Homo sapiens

<400> 15
Leu Pro Met Leu Pro Met
1 5

<210> 16
<211> 6
<212> PRT
<213> Homo sapiens

<400> 16
Arg Pro Asp Gly Tyr Asn
1 5

<210> 17
<211> 6
<212> PRT
<213> Homo sapiens

<400> 17
His Phe Leu Pro Met Leu
1 5

205270 592000